

1:	gb_ba1.*
2:	gb_ba2.*
3:	gb_om.*
4:	gb_ov.*
5:	gb_pat.*
6:	gb_ph.*
7:	gb_p11.*
8:	gb_p12.*
9:	gb_p11.*
10:	gb_p12.*
11:	gb_p12.*
12:	gb_ro.*
13:	gb_st.*
14:	gb_sy.*
15:	gb_un.*
16:	em_fun1.*
17:	em_hun1.*
18:	em_hun2.*
19:	em_in.*
20:	em_om.*
21:	em_ov.*
22:	em_ov.*
23:	em_pat.*
24:	em_ph.*
25:	em_p11.*
26:	em_st.*
27:	em_st.*
28:	em_sy.*
29:	em_un.*
30:	em_v1.*
31:	gb_hg1.*
32:	gb_hg2.*
33:	gb_in1.*
34:	gb_in2.*
35:	em_ba1.*
36:	em_ba2.*
37:	em_hun3.*
38:	em_hun4.*
39:	gb_p14.*
40:	gb_pg3.*
41:	gb_hg4.*
42:	gb_hg5.*
43:	gb_hg6.*

44: em\_hgt7.\*  
45: em\_hgt7.\*  
46: em\_hgt2.\*  
47: em\_hum5.\*  
48: em\_hum5.\*  
49: gb\_pl3.\*  
50: gb\_pl5.\*  
51: gb\_hgt8.\*  
52: gb\_hgt9.\*  
53: gb\_hgt10.\*  
54: gb\_hgt11.\*  
55: gb\_hgt12.\*  
56: gb\_hgt13.\*  
57: gb\_hgt14.\*  
58: gb\_hgt3.\*  
59: gb\_hgt15.\*  
60: gb\_hgt16.\*  
61: gb\_hgt17.\*  
62: em\_hgt4.\*  
63: em\_hgt5.\*  
64: em\_hgt6.\*  
65: em\_hgt7.\*  
66: em\_hum6.\*  
67: em\_hum8.\*  
68: gb\_hgt18.\*  
69: gb\_hgt20.\*  
70: gb\_hgt21.\*  
71: gb\_hgt22.\*  
72: gb\_hgt23.\*  
73: gb\_hgt24.\*  
74: gb\_hgt25.\*  
75: gb\_hgt26.\*  
76: gb\_hgt27.\*  
77: gb\_hgt28.\*  
78: gb\_hgt29.\*  
79: gb\_hgt30.\*  
80: gb\_hgt31.\*  
81: gb\_v11.\*  
82: gb\_v12.\*

## SUMMARIES

No.	Score	Query Match	length	DB	ID	Description
1	1201.6	97.5	199556	40	ALI160290	sap
2	258.4	21.0	127766	11	AC005723	Hom sap
3	258.4	21.0	158440	56	AC008437	Hom sap
4	252	20.5	177694	72	AC019358	Hom sap
5	252	20.5	186867	31	AP000902	Hom sap
6	251.6	20.4	155323	68	AC009824	Hom sap
7	250.6	20.3	99294	73	AC008704	Hom sap
8	250.6	20.3	178035	61	AC021852	Hom sap
9	250.6	20.3	179392	75	AC026620	Hom sap
10	250.6	20.3	185380	72	AC015941	Hom sap
11	250.2	20.3	154395	43	AC022290	Hom sap
12	250.2	20.3	201929	40	ALI15177	Hom sap
13	249.4	20.2	128747	11	HS465N24	Hom sap
14	249	20.2	135259	10	AC004590	Human DNP
15	249	20.2	276336	73	AC011498	Hom sap
16	248.8	20.2	118555	41	HSJ908M14	Hom sap
17	248.6	20.2	188165	33	ALI13936	Hom sap
18	248.6	20.2	288755	51	AC020664	Hom sap
19	248.6	20.2	328686	43	AC021094	Hom sap
20	248.4	20.2	90832	11	AC003065	Hom sap
21	248.4	20.2	119843	39	AC005033	Hom sap
22	248.4	20.2	126228	39	AC006543	Hom sap
23	248.4	20.2	172010	67	AC026541	Hom sap
24	248.4	20.2	226916	39	AC005066	Hom sap

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25 248.4 20.2 234523 39 AC006544 , complete
26 248.2 20.1 169645 78 AC0012351
27 248 20.1 157954 71 AC026284 Homo sapi
28 247.8 20.1 124095 40 AC002477 Homo sapi
29 247.8 20.1 238634 50 CENS01DVX
30 247.6 20.1 63369 41 AC002413
31 247.6 20.1 171031 61 AC0024503
32 247.6 20.1 183059 32 CENS01DRP
33 247.4 20.1 108803 10 HS550H1
34 247.4 20.1 141192 32 AL138795
35 247.2 20.1 172489 41 HSDJ53A19
36 247.2 20.1 179714 32 AL137058
37 247 20.0 29848 39 U73023
38 247 20.0 141771 32 AL138842
39 247 20.0 156493 41 HSDJ533F4
40 246.8 20.0 36384 11 AC004178 Homo sapi
41 246.8 20.0 37760 11 AC004174
42 246.8 20.0 93373 39 AC004084 Homo sapi
43 246.8 20.0 175507 11 CENS01RGB
44 246.8 20.0 178810 68 AC025317
45 246.6 20.0 155446 73 AC021506 Homo sapi

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## ALIGNMENTS

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RESULT 1
LOCUS ALL60290 199356 bp DNA HTG 20-APR-2000
DEFINITION Homo-sapiens chromosome 10 clone RP11-33801, *** SEQUENCING IN
ACCESSION AL160290.3 GI:7634892
VERSION AL160290.3
KEYWORDS HTG; HTGS; PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

## REFERENCE

```

AUTHOR [REDACTED] Sanger Centre, Hinxton, Cambridgeshire,
TITLE [REDACTED] 1 to 199356)
JOURNAL [REDACTED]

```

COMMENT On Apr 22, 2000 this sequence version replaced gi:7263473.

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquerry@sanger.ac.uk

Project Information

Center project name: BA33801

Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 174153 bases at least Q40

Consensus quality: 182105 bases at least Q30

Consensus quality: 188197 bases at least Q20

Insert size: 195356; sum-of-ctrls

Insert size: 195260; 7.3% error; agarose-fp

Quality coverage: 2.91x in Q20 bases; sum-of-ctrls Quality

Quality coverage: 2.91x in Q20 bases; agarose-fp

Quality coverage: 2.91x in Q20 bases; agarose-fp

Quality coverage: 2.91x in Q20 bases; agarose-fp

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Quality coverage: 2.91x in Q20 bases; agarose-fp

Quality coverage: 2.91x in Q20 bases; agarose-fp

Quality coverage: 2.91x in Q20 bases; agarose-fp

pieces within a fragment\_chain is reflected in \* this file. Gaps between the contigs are represented as \* runs of N, but the exact sizes of the gaps are unknown. \* This record will be updated with the finished sequence as \* soon as it is available and the accession number will be \* preserved.

```

1 1854 1753 contig of 1753 bp in length; fragment_chain 1 *
1 3045 4246 contig of 1202 bp in length; fragment_chain 2 *
4347 6506 contig of 2160 bp in length; fragment_chain 2 *
6607 13314 contig of 6708 bp in length; fragment_chain 2 *
13415 24031 contig of 10617 bp in length; fragment_chain 2 *
24132 28251 contig of 4130 bp in length; fragment_chain 2 *
28362 31321 contig of 2960 bp in length; fragment_chain 3 *
31422 37131 contig of 5710 bp in length; fragment_chain 3 *
40096 contig of 2865 bp in length; fragment_chain 3 *
40197 43016 contig of 2820 bp in length; fragment_chain 3 *
43117 44385 contig of 1269 bp in length; fragment_chain 3 *
44486 51780 contig of 7295 bp in length; fragment_chain 4 *
51881 58176 contig of 6296 bp in length; fragment_chain 4 *
58277 59411 contig of 1135 bp in length; fragment_chain 4 *
59512 70018 contig of 10507 bp in length; fragment_chain 5 *
70119 72021 contig of 6903 bp in length; fragment_chain 5 *
72122 79576 contig of 2455 bp in length; fragment_chain 5 *
79677 81979 contig of 2303 bp in length; fragment_chain 6 *
82080 83547 contig of 1468 bp in length; fragment_chain 6 *
83648 85785 contig of 2138 bp in length; fragment_chain 7 *
85886 96338 contig of 10453 bp in length; fragment_chain 8 *
96439 104736 contig of 8298 bp in length; fragment_chain 8 *
104837 111369 contig of 6533 bp in length; fragment_chain 9 *
111470 122050 contig of 10581 bp in length; fragment_chain 9 *
122151 123896 contig of 1746 bp in length; fragment_chain 10 *
123997 129043 contig of 5047 bp in length; fragment_chain 10 *
129144 132013 contig of 2870 bp in length; fragment_chain 10 *
132114 138452 contig of 6339 bp in length
138553 140132 contig of 1580 bp in length
140233 145011 contig of 4779 bp in length
145112 146294 contig of 1183 bp in length
146395 152223 contig of 5829 bp in length
152324 156610 contig of 4287 bp in length
156711 163543 contig of 6933 bp in length
163744 167586 contig of 3843 bp in length
167687 175411 contig of 7725 bp in length; fragment_chain 11
175512 181689 contig of 6178 bp in length; fragment_chain 11
181790 185683 contig of 3894 bp in length; fragment_chain 11
185784 188664 contig of 2881 bp in length; fragment_chain 11
188765 199356 contig of 10592 bp in length; fragment_chain 11

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## FEATURES

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/db\_xref="taxon:9606"

/chromosome="10"

/clone="RP11-33801"

/clone.lib="RPCT-11.2"

1. 1753

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fragment\_chain:1

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/note="assembly-fragment:00499"

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/note="assembly-fragment:00060"

fragment\_chain:2"

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fragment\_chain:2"

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misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

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28362..31321
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85886..96338
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104837..111369
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111470..122050
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122151..123896
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fragment_chain:10"
123997..129043
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145112..146294
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146395..152223
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152324..156610
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Query Match 97.5% Score 1201.6; DB 40; Length 199356;
Best Local Similarity 99.7% Pred No. 0;
Matches 1204; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 17 gtcagaagacaccttgaactacacagaagattatatacagctcttcatgaagaccagcaa 76
|||||
DB 33957 gctcagAACACCTTGACTGACACAGAGATTATACCAAGTCTTTCATCCAGAGCCACCA 34016
|||||

QY 77 ccactgtctatactgtctctcccccacagactcaagcatcctcagggaagggaac 136
|||||
DB 34017 CCACGTGCTCATACAGTTCTTCCCNCCNACNACTTGACATCCTTCGAGGAAAGGAGACC 34076
|||||

QY 137 agaaacagagaccatcttcaactgacgacgacgacacatcccttgaagcatgacatgac 196
|||||
DB 34077 ACACAGGCGACCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 34136
|||||

QY 197 tccctgaagctgtctcaagtgagagcgaacgacacatcccttgaagcatgagacacat 256
|||||
DB 34137 TCCTGACAGCTGCTCAGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34196
|||||

QY 257 taacacagatgacagaacctgacatgacatcccttgaagcatgagacacatgacacacac 316
|||||
DB 34197 TACACAGATGACAGAACTGACATGCTCCCTTTGAGTCCCAACATAGTGACACACC 34256
|||||

QY 317 tctcaattgccccagaagaagagccctgagcacaacagacatgacatctgtctgacacaaa 376
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DB 34257 TGTCAATTTCCCAAGAAAGAGACCTGAGCCACACACATCTTCTGCTCACACAAA 34316
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QY 377 acaagagatgctcgcggaagaataatgaagagagaatttgcttgccttgccttgccttgcct 436
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DB 34317 ACAGGATGCTCGGGAGAAATATGAAGAGAAATTTGCTTGGCTTGGCTTGGCTTGGCTTGGCT 34376
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QY 437 accacataggttcgcgtctgacatgacatgacatgacatgacatgacatgacatgacatgac 496
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DB 34377 ACCACATAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 34436
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QY 497 gtagtctgacatgacagacacacacacacacacacacacacacacacacacacacacacac 556
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DB 34437 GTGCTGTATGACAGACACACACACACACACACACACACACACACACACACACACACACAC 34496
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QY 557 agagttgacagccttccctgtctacacagacacacacacacacacacacacacacacacacac 616
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DB 34497 AAGATTGCCAGCTTTCCTGCTTACACAGACCATGAGAGTCCAGCCATACATGTCATGTG 34556
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QY 617 gcccaacacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 676
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DB 34557 GCCCAACCATGACATGAGAGAACTGCGAGAGACTTACAGAGCCAGCTTGGGTGTAG 34616
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QY 677 aaacatcacatagacacacacacacacacacacacacacacacacacacacacacacacacac 736
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DB 34617 AAACATACATAGACACAAAGAACTCACTGTGTCTTCAAGAGTCAAGGCTTGTAGAC 34676
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QY 737 agtatcatctacacagacacacacacacacacacacacacacacacacacacacacacacacac 796
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DB 34677 AGTATCATCTCACACAGACATTCAAATTTGATCTTCTTGTGAGGCCAGAGGCTGAA 34736
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QY 797 tctggaagacacacacacacacacacacacacacacacacacacacacacacacacacacacacacac 856
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QY 857 cacatgacatgcttagaggtgtgacgaggtgtgagagccttgcacacacacacacacacacacacac 916
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